

Genome version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003 16:40:42 : Search time 14.214 Seconds
(without alignments)
56.542 Million cell updates/sec

Title: US-09-856-070-18
Perfect score: 24
Sequence: 1 KEELM 5

Scoring table: BLASTSUM62
Gapop 10 0 . Gapext 0 5

Searched: 671580 seqs, 26047116 residues 671580
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL21.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-ordaealle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-virus.*
- 16: sp-bacteriap.*
- 17: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	24	100.0	95	2 Q86671	Q86671 bacillus me
2	24	100.0	96	17 Q8U114	Q8U114 pyrococcus
3	24	100.0	97	16 Q4K20	Q4K20 chlamydia t
4	24	100.0	112	16 Q8XJP2	Q8XJP2 clostridium
5	24	100.0	113	5 Q77163	Q77163 equimoeba i
6	24	100.0	121	16 Q8V612	Q8V612 listeria mo
7	24	100.0	124	4 Q9N1N7	Q9N1N7 homo sapien
8	24	100.0	135	17 Q9E2P1	Q9E2P1 sulfolobus
9	24	100.0	146	4 Q9RPX7	Q9RPX7 homo sapien
10	24	100.0	152	4 Q9U122	Q9U122 homo sapien
11	24	100.0	156	4 Q9U128	Q9U128 homo sapien
12	24	100.0	159	4 Q9U127	Q9U127 homo sapien
13	24	100.0	159	4 Q9U126	Q9U126 homo sapien
14	24	100.0	159	16 Q9U115	Q9U115 fusbobacteri
15	24	100.0	161	4 Q9K20	Q9K20 homo sapien
16	24	100.0	164	16 Q8RGP5	Q8RGP5 fusbobacteri

17	24	100.0	168	12 Q89174	Q89174 variola vir
18	24	100.0	168	12 Q57237	Q57237 vaccinia vi
19	24	100.0	168	12 Q57237	Q57237 vaccinia vi
20	24	100.0	168	12 Q89521	Q89521 canicpox vi
21	24	100.0	168	12 Q8QMR9	Q8QMR9 cowpox viru
22	24	100.0	174	4 Q9HSN3	Q9HSN3 homo sapien
23	24	100.0	195	10 Q94712	Q94712 arabidopsis
24	24	100.0	196	17 Q9V307	Q9V307 pyrococcus
25	24	100.0	197	17 Q51141	Q51141 pyrococcus
26	24	100.0	203	5 Q83W55	Q83W55 encephalito
27	24	100.0	204	16 Q8K674	Q8K674 fusbobacteri
28	24	100.0	204	17 Q9HHA3	Q9HHA3 pyrococcus
29	24	100.0	216	14 Q9E5F9	Q9E5F9 lola rubrip
30	24	100.0	217	5 Q31262	Q31262 caenorhabdi
31	24	100.0	226	16 Q8UKT2	Q8UKT2 agrobacteri
32	24	100.0	273	17 Q59396	Q59396 pyrococcus
33	24	100.0	273	17 Q8U482	Q8U482 pyrococcus
34	24	100.0	275	17 Q975V8	Q975V8 sulfolobus
35	24	100.0	284	4 Q36MW7	Q36MW7 homo sapien
36	24	100.0	300	17 Q9HKH0	Q9HKH0 thermoplasm
37	24	100.0	305	4 Q9H278	Q9H278 homo sapien
38	24	100.0	311	4 Q9HSB6	Q9HSB6 homo sapien
39	24	100.0	311	14 Q9Q2P2	Q9Q2P2 streptococ
40	24	100.0	328	12 Q88438	Q88438 strawberri
41	24	100.0	329	12 Q9DK00	Q9DK00 elephant he
42	24	100.0	338	19 Q5S261	Q5S261 arabidopsis
43	24	100.0	340	19 Q82738	Q82738 arabidopsis
44	24	100.0	343	2 Q9S035	Q9S035 borrelia bu
45	24	100.0	344	16 Q98QC3	Q98QC3 mycoplasma

ALIGNMENTS

RESULT 1

ID Q68671 PRELIMINARY: PPT: 95 AA.

AC Q68671: DT 01-AUG-1998 (TREMREL. 07, Created)
DI 01-AUG-1998 (TREMREL. 07, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE Gas vesicle protein Gvps.
GN GVPs.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
CC Bacillaceae; Bacillus.
OX NCBI TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VT1660;
RX MEDLINE=98233742; PubMed=9573198;
RA Li N., Cannon M.C.;
RT "Gas vesicle genes identified in Bacillus megaterium and functional
expression in Escherichia coli.";
PL J. Bacteriol. 180:2450-2458(1998).
DR EMBL: AF054765; AAC38410.1;
DR InterPro: IPR000638; Gas_vesicle.
DR Pfam: PF00741; Gas_vesicle; 1.
DR ProDom: PD003598; Gas_vesicle; 1.
SQ SEQUENCE: 95 AA; 10422 MW: 10422 MW: ACPAEPF27DE60B QPC64;

Query Match 100.0%; Score 24; DB 2; Length 95;

Best Local Similarity 100.0%; Freq. No. 1; E=0.02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Q7 1 KEELM 5
|||||
Db /5 KEELM 80

RESULT 2

Q8U114 PRELIMINARY: PPT: 96 AA.

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AC O88114;
DI 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PE1192.
GN PE1192.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V-1 / DSM 4648 / ATCC 4567 / DSM 8422.
RA Weiss R.B., Dunn D.M., Robb P.L., Brown J.R.;
RI "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/CCDS databases
DR EMBL: AF010227; AAC81316.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA: 11076 MW: 903666AFRRGQF74 CRG64;
Query Match 100.0%; Score 24; DB 17; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 17 KEELM 21

RESULT 4
ID O84663 PRELIMINARY; PRT: 97 AA.
AC O84663;
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein C1656.
GN C1656.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales, Chlamydiaceae, Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/OW-3/CX;
RA MEDLINE=9500809; PubMed=9744136;
RA Stephens R.S., Kalman S., Lammel C., Fan J., Marathe P., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RI "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
DR EMBL: AF001346; AAC68251.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 97 AA: 11164 MW: 903656SP20149PS1 CRG64;
Query Match 100.0%; Score 24; DB 16; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 24 KEELM 28

RESULT 4
Q8XJP2 PRELIMINARY; PRT: 112 AA.
ID Q8XJP2;
AC Q8XJP2;
DI 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein GPE1714.
GN GPE1714.

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OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RC PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.;
RI "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL FEMS Microbiol. Lett. 201:201-205(2001).
DR EMBL: AP003191; BAB81420.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 112 AA: 12440 MW: 101094A6D81HAFFD CRG64;
Query Match 100.0%; Score 24; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 81 KEELM 85

RESULT 5
ID O77163 PRELIMINARY; PRT: 113 AA.
AC O77163;
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ADP-ribosylation factor (Fragment).
GN ADF.
OS Entamoeba invadens.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=33085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP-1;
RC MEDLINE=99270976; PubMed=10338523;
RA Ghosh S.K., Field J., Frisardi M., Rosenthal B., Mai Z., Rogers R.,
RA Samuelson J.;
RI "Chitinase secretion by encysting Entamoeba invadens and transfect
RT Entamoeba histolytica trophozoites: localization of secretory
RL vesicles, endoplasmic reticulum, and Golgi apparatus."
DR EMBL: AF082518; AAC64064.1; -.
DR HSSP; P32889; IRRF.
DR InterPro; IPR000251; ARF_family.
DR InterPro; IPR002046; Sar1_GTPBP.
DR Pfam; PF00025; arf; 1.
DR PRINTS; PP00328; SAR1GTPBP.
DR SMART; SM00177; ARF; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA: 12991 MW: 64A1CF5451D1D4A6 CRG64;
Query Match 100.0%; Score 24; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 86 KEELM 90

RESULT 6
Q8Y612 PRELIMINARY; PRT: 121 AA.
ID Q8Y612;
AC Q8Y612;
DI 01-MAR-2002 (TrEMBLrel. 20, Created)

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DI 01-MAR-2002 (TREMBlrel. 20, last sequence update)
 DI 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Hypothetical protein lmo1890.
 GN Lmo1890.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCHI_TaxID=1639;
 RN [1]
 PP SEQUENCE FROM N.A.
 PC STRAIN-EGD-E / SEROVAP 1/2A;
 RX MEDLINE=21537279; PubMed=1470669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,
 RA Charif A., Chetoui F., Gave F., de Patouat A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud F., Durapt L., Dussurget O.,
 PA Entian K.-D., Fshih H., Garcia-del Portillo F., Garido P.,
 RA Gautier L., Geisel W., Gomez Lopez N., Hain T., Hauf J., Jackson B.,
 RA Jones L.-M., Kastrup U., Klotz J., Kuhn M., Kist P., Korapkar G.,
 RA Madico E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Varquez-Bolland J. A., Voss H., Wehland J., Gossart F.,
 RT *Comparative genomics of Listeria species.*;
 RL Science 294:849-852(2001)
 DR EMBL: AL591981; CAC99468.1; -;
 DR LocusList: LMO01890; -;
 KW Hypothetical protein. Complete proteome.
 SQ SEQUENCE 121 AA; 14517 MW; 5EE201A36C170248 CRC64;
 Query Match 100.0%; Score 24; DB 4; Length 121;
 Host Local Similarity 100.0%; Pred. No. 1 8e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 Db 117 KEELM 121
 RESULT 7
 Q9NTN7
 ID Q9NTN7 PRELIMINARY: PPT; 124 AA.
 AC Q9NTN7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DI 01-SEP-2001 (TREMBlrel. 19, last annotation update)
 DE DJ207F6.1 (Novel nucleolar protein NOP56 like protein)
 DF (Fragment)
 GN DJ207F6.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCHI_TaxID=9606;
 RN [1]
 PP SEQUENCE FROM N.A.
 RA Griffiths G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL13258; CAB92070.1; -;
 DR InterPro: IPR000873; AMP-BIND.
 DR PROSITE: PS00455; AMP-BINDING.
 FI NON_TER 1
 SQ SEQUENCE 124 AA; 13898 MW; 263A046C3560622C CRC64;
 Query Match 100.0%; Score 24; DB 4; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1 4e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 Db 44 KEELM 48
 RESULT 8

Q96ZEL
 ID Q96ZEL PRELIMINARY: PPT; 135 AA.
 AC Q96ZEL;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DI 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Putative transcriptional regulator.
 GN S01890.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OX NCHI_TaxID=111955;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN-JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin no K., Takahashi M.,
 RA Sakino M., Baba S.-I., Akai A., Kosugi H., Haseyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka P., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki I., Koshida N., Oguchi A.,
 RA Aoki K. I., Masuda S., Yanaqili M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT *Complete genome sequence of an aerobic thermophilic
 RC Crenarchaeon, Sulfolobus tokodaii strain 7.*;
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000044; HA66984.1; -;
 KW Hypothetical protein. Complete proteome.
 SQ SEQUENCE 135 AA; 15654 MW; 9d18AA9B49D2FAC2 CRC64;
 Query Match 100.0%; Score 24; DB 17; Length 135;
 Host Local Similarity 100.0%; Pred. No. 2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 Db 103 KEELM 107
 RESULT 9
 Q9BRX7
 ID Q9BRX7 PRELIMINARY: PPT; 146 AA.
 AC Q9BRX7;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DI 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hypothetical 14 kD protein (m6000) (Fract. 102 M600017).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCHI_TaxID=9606;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 PP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Strausberg R.;
 KL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005872; AA05872.1; -;
 DR EMBL: BC011498; AA011498.1; -;
 DP InterPro: IPR000286; His_deacetylase.
 DR Pfam: PF00850; His_deacetylase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 146 AA; 16439 MW; 6A2C126D7E1F84B5 CRC64;
 Query Match 100.0%; Score 24; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 Db 1111

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DB 148 KEELM 142

RESULT 10
Q9UJZ6
AC Q9UJZ6 PRELIMINARY: PRT: 152 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytoovillin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Chen Z.C., Fadiel A., Nattoli F.;
RL "Mutation of cytoovillin gene in glioblastoma.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF190059; AAF03158.1; -
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA: 18416 MW: 87081700.291 CRC64;

Query Match 100.0%; Score 24; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 144 KEELM 148

RESULT 11
Q9UJZ8
AC Q9UJZ8 PRELIMINARY: PRT: 156 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Chen Z.C., Fadiel A., Nattoli F.;
RL "Mutation of ezrin gene in cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188896; AAF03154.1; -
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA: 19642 MW: 15955AA684203A6 CRC64;

Query Match 100.0%; Score 24; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 144 KEELM 148

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DB 148 KEELM 152

RESULT 12
Q9UJZ7
AC Q9UJZ7 PRELIMINARY: PRT: 158 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Chen Z.C., Fadiel A., Nattoli F.;
RL "Ezrin gene mutation in ovarian cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188897; AAF03155.1; -
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA: 19086 MW: 8692F1HC6F2957E CRC64;

Query Match 100.0%; Score 24; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 147 KEELM 151

RESULT 13
Q9UJZ6
AC Q9UJZ6 PRELIMINARY: PRT: 159 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Fadiel A., Chen Z.C., Nattoli F.;
RL "Mutation of ezrin gene in cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189213; AAF03156.1; -
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA: 19234 MW: 7C398488B7BA70FA CRC64;

Query Match 100.0%; Score 24; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|||||
DB 147 KEELM 151

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Search completed: January 16, 2003, 16:55:41
Job Time : 20.2143 secs

RESULT 14

Q8RII5 PRELIMINARY: PRT: 159 AA.
AC Q8RII5
DI 01-JUN-2002 (FEMBLrel. 21, Created)
DI 01-JUN-2002 (FEMBLrel. 21, last sequence update)
DI 01-JUN-2002 (FEMBLrel. 21, last annotation update)
DE Competence protein.
GN FN1611.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 25586;
RX MEDLINE-21886394; PubMed-11889109;
RA Kapral V., Anderson J., Ivancova N., Reznik G., Los T., Lykedis A.,
RA Bhattacharya A., Hartman A., Gardner W., Greshkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Hernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fongstein M., Kyriades N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
PI J. Bacteriol. 184:2005-2018(2002).
PK EMBL: AF010469; AAL93726.1; -.
KW Complete proteome.
SQ SEQUENCE 159 AA: 18634 MW: 16159F46C3B3DB6 CRC64;

Query Match 100.0%; Score 24; DH 16; Length 159;
Host local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
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DB 25 KEELM 29

RESULT 15

Q9UK20 PRELIMINARY: PRT: 161 AA.
AC Q9UK20
DI 01-MAY-2000 (FEMBLrel. 13, Created)
DI 01-MAY-2000 (FEMBLrel. 13, last sequence update)
DI 01-MAR-2002 (FEMBLrel. 20, last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RA Chen Z.C., Fadiel A., Naftolin F.;
RI "Mutation analysis of ezrin gene in cancer cells.";
RI Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF187552; AAD56713.1; -.
DR InterPro: IPR000294; Band_4 1.
DR Pfam: PF00373; Band_41; 1.
DR Pfam: PF00769; ERW; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1 1
FT NON_TER 161 161
SQ SEQUENCE 161 AA: 19436 MW: 5F06F6910E017099 CRC64;

Query Match 100.0%; Score 24; DB 4; Length 161;
Host local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
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DB 153 KEELM 157

